

The maintenance of genetic variation in polygenic sexually antagonistic traits

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Selection often favours different characteristics in males and females, leading to genetic conflicts across the sexes. Theory suggests that these conflicts can maintain genetic variation by generating balancing selection, especially under specific patterns of allelic dominance. However, so far, most of this theory has neglected the genetic complexity of polygenic traits, where phenotypes may be determined collectively by alleles carried across many genetic loci. Consequently, the influence of sexual antagonism on genetic variation in the many traits that show such multilocus genetic architecture remains poorly understood. Here, we use mathematical modelling and computer simulations to investigate the evolution of a polygenic trait that has different optima in males and females. We show that the conditions necessary to maintain variation across multiple loci are significantly more restrictive than at a single locus, with very strong sexual conflict typically required. This is because fitness landscapes that typically favour polymorphism at a single locus (through their effects on dominance), also generate patterns of epistasis across the loci encoding a polygenic trait, with such interactions tending to favour the fixation of a single genotype. Together our results indicate that sex-specific selection is not a straightforward source of balancing selection in polygenic traits, and that instead sexual antagonism should be most prolific in maintaining genetic variation when traits are determined by a single large effect locus.